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SEQUENCE LISTING
<110> Roche Diagnostics GmbH
        Expression of alkaline phosphatase in yeast
<130> 5387/00/
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<160> 38
<170> PatentIn Ver. 2.1
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<211> 1476
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<213> Bovine
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ttcttggggg atgggatggg ggtgcctacg gtgacagcca ctcggatcct aaaggggcag 180
atgaatggca aactgggacc tgagacaccc ctggccatgg accagttccc atacgtggct 240
ctgtccaaga catacaacgt ggacagacag gtgccagaca gcgcaggcac tgccactgcc 300
tacctgtgtg gggtcaaggg caactacaga accatcggtg taagtgcagc cgcccqctac 360
aatcagtgca acacgacacg tgggaatgag gtcacgtctg tgatcaaccg ggccaagaaa 420
geagggaagg cegtgggagt ggtgaceace accagggtge ageatgeete ceeageeggg 480
gcctacgcgc acacggtgaa ccgaaactgg tactcagacg ccgacctgcc tgctgatgca 540
cagaagaatg getgecagga categeegea cagetggtet acaacatgga tattgacgtg 600
atcotgggtg gaggccgaat gtacatgttt cctgagggga ccccagaccc tgaataccca 660
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gccaagcacc agggagccca gtatgtgtgg aaccgcactg cgctccttca ggcggccgat 780
gactccagtg taacacact catgggcctc tttgagccgg cagacatgaa gtataatgtt 840
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teccatgtet tetettttgg tggetacaea etgegtggga eetecatttt eggtetggee 1140
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<213> Bovine
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Ala Lys Asn Val Ile Leu Phe Leu Gly Asp Gly Met Gly Val Pro Thr
Val Thr Ala Thr Arg Ile Leu Lys Gly Gln Met Asn Gly Lys Leu Gly
     50
                         55
Pro Glu Thr Pro Leu Ala Met Asp Gln Phe Pro Tyr Val Ala Leu Ser
Lys Thr Tyr Asn Val Asp Arg Gln Val Pro Asp Ser Ala Gly Thr Ala
Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Tyr Arg Thr Ile Gly Val
Ser Ala Ala Arg Tyr Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu
Val Thr Ser Val Ile Asn Arg Ala Lys Lys Ala Gly Lys Ala Val Gly
                        135
Val Val Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Ala Tyr
145
Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Leu Pro Ala
                                    170
Asp Ala Gln Lys Asn Gly Cys Gln Asp Ile Ala Ala Gln Leu Val Tyr
Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Met Tyr Met Phe
                            200
Pro Glu Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Ala Ser Val Asn
Gly Val Arg Lys Asp Lys Gln Asn Leu Val Gln Glu Trp Gln Ala Lys
                    230
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His Gln Gly Ala Gln Tyr Val Trp Asn Arg Thr Ala Leu Leu Gln Ala 245 250 255

Ala Asp Asp Ser Ser Val Thr His Leu Met Gly Leu Phe Glu Pro Ala 260 265 270

Asp Met Lys Tyr Asn Val Gln Gln Asp His Thr Lys Asp Pro Thr Leu 275 280 285

Ala Glu Met Thr Glu Ala Ala Leu Gln Val Leu Ser Arg Asn Pro Arg 290 295 300

Gly Phe Tyr Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His His 305 310 315 320

Asp Gly Lys Ala Tyr Met Ala Leu Thr Glu Ala Ile Met Phe Asp Asn 325 330 335

Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile 340 345 350

Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr 355 360 365

Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp 370 380

Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala 385 390 395 400

Leu Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu 405 410 415

Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His 420 425 430

Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu 435 440 445

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tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa 180
atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct 240
ttgtctaaga cttacaatgt tgatagacaa gttccagatt ctgctggtac tgctactgct 300
tacttgtgtg gtgttaaggg taattacaga actattggtg tttctgctgc tgctagatac 360
aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag 420
gctggtaagg ctgttggtgt tgttactact actagagttc aacatgcttc tccagctggt 480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct 540
caaaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatgtt 600
attttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca 660
gatgatgctt ctgttaatgg tgttagaaag gataagcaaa atttggttca agaatggcaa 720
gctaagcatc aaggtgctca atatgtttgg aatagaactg ctttgttgca agctgctgat 780
gattctagtg ttactcattt gatgggtttg tttgaaccag ctgatatgaa gtataatgtt 840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt 900
ttgtctagaa atccaagagg tttttacttg tttgttgaag gtggtagaat tgatcatggt 960
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gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat 1080
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tatgetttgg gtggtggtte tagaccagat gttaatggta gtactagtga agaaccatet 1260
tacagacaac aagctgctgt tccattggct agtgaaactc atggtggtga agatgttgct 1320
gtttttgcta gaggtccaca agctcatttg gttcatggtg ttcaagaaga aacttttgtt 1380
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<211> 70
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Artificial
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<210> 8
<211> 69
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Artificial
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tttgaaggg
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<210> 9
<211> 70
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aaaattctag
<210> 10
<211> 71
<212> DNA
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<211> 71
<212> DNA
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<210> 12
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<223> Description of Artificial Sequence: Artificial
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 catactgtta atag
 <210> 15
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	Z210× 10	
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	taacaccatt aac	73
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<210> 25
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gatcagcagt aac
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<211> 77
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<223> Description of Artificial Sequence: Artificial
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gctagtgaaa ctcatgg
<210> 31
<211> 73
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<400> 31
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ggttgtgttg aacc
<210> 33
<211> 82
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<210> 34
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     <211> 10
      <212> PRT
: []
      <213> Saccharomyces cerevisiae
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.
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                         5
from
from
Yan Reit Can Bank
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